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Protein-Lipid Interactions

Edited by **A. Watts**

New Comprehensive Biochemistry Volume 25

Protein-lipid interactions as a field of study is now a mature area, and this volume of *New Comprehensive Biochemistry* has been published with two objectives in mind. Firstly, to look to the future, and try to envisage how the subject may develop in the near to medium future. Secondly, to present contrasting or complementary views on the same system. For example, the acetylcholine receptor is discussed from a predominantly structural aspect by Barrantes, and from the kinetic standpoint by Rankin, et al.

The volume not only gives an update on specific aspects of the field, but also shows the way in which the phenomenon of protein-lipid interactions is now seemingly infiltrating many areas of biomembrane research, from recombinant DNA studies, protein insertion and assembly and reconstitution considerations to structural studies of membrane proteins.

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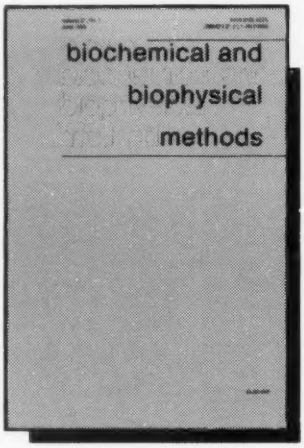

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[1] Diller, R., Stockburger, M., Oesterhelt, D. and Tittor, J. (1987) FEBS Lett. 217, 297-304.

[2] Gomperts, B.D. and Fewtrell, C.M.S. (1985) in: Molecular Mechanisms of Transmembrane Signalling (Cohen, P. and Houslay, M.D. eds) Mol. Aspects Cell. Regul. vol. 4, pp. 377–409, Elsevier, Amsterdam, New York.

[3] Robson, B. and Garnier, J. (1986) Introduction to Proteins and Protein Engineering, Elsevier, Amsterdam, New York.

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3.2. *Nucleic and amino acid sequences* should be submitted as sharp, clean prints already reduced as much as possible to fit within a single-column (8.4 cm) or double-column width (17.6 cm), while retaining perfect legibility (e.g. to avoid confusion between the letters C and G). If a word-processor is used to generate the sequences, a letter-quality printer should be employed; matrix-printed characters do not reproduce.
In reporting DNA sequences, presentation of a sequencing strategy is generally unnecessary. However, it should be confirmed by a statement in the Materials and Methods section that the sequence was determined on both strands.

3.3. Original half-tone figures should be very sharp, high-contrast photoprints and be designed to display relevant information only, avoiding disproportionately large labelling of lanes. Line drawings should not be included in half-tone figures. For photographs which require labels, such as electrophoretograms, please supply the initial photographs mounted on white paper with lettering. Do NOT send photographs of photographs.

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△ ▽ ◇ □ ⊙ ⊖ ⊕ ▫ ☆ ▲ ▼ ◆ • ■ ★ × +

3.5. When preparing figures, particularly graphs, we urge authors to follow the suggestions of H.G. Hers ((1984) Nature 307, 205). In particular:
(1) Graph with more than one line: identify each by appropriate labelling. **(2)** Figure containing several panels with the same axes, usually denoted a,b, etc: indicate on each panel its experimental specificity. **(3)** Use one symbol for the same experimental condition in all comparable figures in the article. **(4)** If several symbols necessary: use the open circle (suggesting nothing added) for the control, e.g. experiment without (○) or with (●) an addition or treatment. **(5)** Label axes as precisely as possible: e.g. 'Time after drug addition' rather than 'Time'. Also express results in mol rather than cpm or absorbance units, sparing readers the task of conversion. If results are given in percent, define 100% in standard units in the legend. **(6)** *Legend:* should be as short as possible, and could often be restricted to the title since, ideally, the figure would be intelligible without referring to the legend.

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